

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

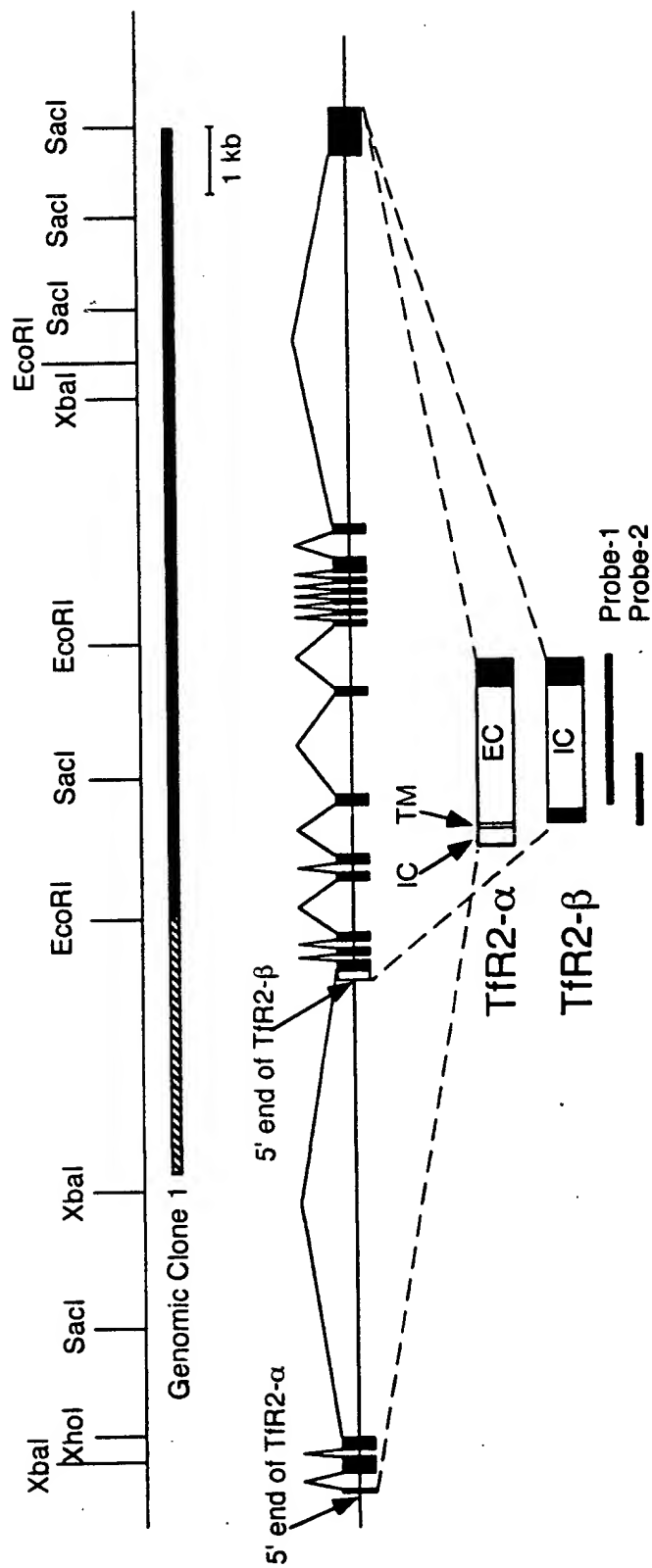
Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.

FIG. 1



Exon 3 of TfR2- α

CCTTCCTACTGGGCTACGTCGCCTTCCGAGGGTCCTGCCAGGCGTGCGGAGACTCTGTGT
 TGGTGGTCAGTGAGGATGTCAACTATGAGCCTGACCTGGATTTCACCAGGGCAGACTCT
 ACTGGAGCGACCTCCAGGCCATGTTCTGCAGTTCCTGGGGGAGGGGCGCCTGGAGGACA
 CCATCAG

Primer-D

Exon 4 (boxed sequence is in the TfR2- β only)

GCGTCCGCGGGGAGCGCTCTTTTCCTAAACTCAGGAACCCCTCGCCGCCCTGCCCCCTGG
 CGACCCACGTCTCTGGCATCCTTCCCTCTTCCCTCCCTCTCCTCCGGGCGCCCAAAAAA
 GTCCCCACCTCTCCCCGCTTAGGCAAACCAGCCTTCGGGAACGGGTGGCAGGCTCGGCCG
 GGATGGCCGCTCTGACTCAGGACATTCGCGCGGCGCTCTCCCGCCAGAAGCTGGACCACG
 TGTGGACCGACACGCACTACGTGGGGCTGCAATTCCCGGATCC

Primer-C

Primer-A

Exon 5 (common for both α - and β -forms)

GGCTCACCCCAACACCCTGCACTGGGTCGATGAGGCCGGGAAGGTCGGAGAGCAGCTGCC
 GCTGGAGGACCCTGACGTCTACTGCCCCTACAGCGCCATCGGCAACGTCACG

Primer-E

FIG. 3

TIR2-α 1 MERLWGLFQRALQLSPSSQTVYQAVEGPRKGHLEELLEDGEEGAETLAH
 TIR 1 M---MDQARSAFSNLFGGEPLSYTRFSLAR-----QVDGONS
 PSMA 1 M-----

TIR2-α 51 FCPMELRGPEPLGSRPRQPNLI PWAAAGRRAAPYLVLTALLIFTGAFLLG
 TIR 35 HVEMKLAVDEENADNNTKANVTKPKRCSGSICYGTIAVIVFFLIGFMIG
 PSMA 2 -----WNL LHETDSAVATARRRPRWLCAGALVLAGGFLLG

TIR2-α 101 YVAF-RGSC-QACGDSVLVSEDEVNYPEDLDFHQGR-LYWSDLQAMFLQF
 TIR 85 YLG YCKGVEPKTECERLAGTESPVREEPGEDFPAARRLYWDDLKRKLSK
 PSMA 37 FLF--GWFIKSSNEATNITPKHNMKA-----F

TIR2-α 148 LGEGRLED TIR--QTS LRE R VAGSAGMAALTQD LRAALS RQKLDH VWT D
 TIR 135 LDSTDFSTIKLLNENS YVPREAGSQKDENLALYVENQFREFKLSKVWRD
 PSMA 62 LDELKAENIKKFLYNFTQIPHLAGTEQNFQLAKQIQSQWKEFGLDSEVLA

TIR2-α 195 THYVGLQF-PDPAHPNTLHWVDEAGKVGEQ--LPLEDPDVYCPYSAIGNV
 TIR 185 QHFVKIQV-KDS A-QNSVITVDKNGRLVY--LVENP-GGYVAYSKAATV
 PSMA 112 -HYDVLLSYPNKTHPNYISLINEOGNEIFNTSLFEPPPPGEYENVSDIVPP

TIR2-α 242 T-----GELVYAHYGRPEDLQDLRARGVDPV-GRLLLVRVGVVISF
 TIR 229 T-----GKL V HANFGTKKDFEDL---YTPVNGSIVIVRAGKITF
 PSMA 161 FSAFSPQGMPEGDLVYVNYARTEDFFKLIERDMKINCSGKIVIAARYGKVFR

TIR2-α 281 AQKVTNAQDFGAQGVLIYPEPAD-FSQDPPKPSLSSQQA VYGHVH-----
 TIR 265 AEKVANAESLNAIGVLIYMDQTK-F-PIVNAE-----LSFFGHAH-----
 PSMA 211 GNKVKNAQLAGAKGVILYSDPADYFAPGVKSYPDGWNLPGGG VQVRGNILN

TIR2-α 325 L-GTGDPYTPGFPSFNQTQFPPIVA-SSGLPSIPAQPI SADIASRLRLRKLK
 TIR 303 L-GTGDPYTPGFPSFNHTQFPPIVA-SSGLPNIIPVQTI SRAAAEKLFGNME
 PSMA 261 LNAAGDPLTPGYPAN EYAYRRGIAEAVGLPSIPVHPIGYYDAQKLLKMG

TIR2-α 373 GPVAPQE--WQSSL LGS PYHLGPGPR-----LRLVNNHRTSTPINN
 TIR 351 GD-CPSD--WK-----TDSTCRMVTS ESKNVKLT VSNVLKEIKILN
 PSMA 311 GS-APPDSSWRGSLK-V PYNVGP GF TGNFSTQK-VKMHITHSTNEVTIRIYN

TIR2-α 413 IFGCIEGRSEPDHYVVI GAQRDAWGPGA AKSAVGTAILLELVRTFSSMVS
 TIR 389 IFGVIKGFVEPDHYVVI GAQRDAWGPGA AKSGVGTAILLLKL AQMFSDMVL
 PSMA 358 VIGTLRGAVEPDHYVVI LGGHRDSWVFGGIDPQSGAAV VHEIVRSFGTLKK

TIR2-α 463 N-GFRPRRSLLFISWDGGDFGSVGSTEWLEGYLSVLHLKAVVYVSLDNAV
 TIR 439 KDGFQPSRSIFASWSAGDFGSVGATEWLEGYLSVLHLKAFTYINLDKAV
 PSMA 408 E-GWRPRRTILFASWDAEEFGLLGSTEWAEENSRL LQERGVA YINADSSI

TIR2-α 512 LGDDKFHAKTSPLLTSLIESVLKQVDSPNH--SGQTLYEQVVFTNPSWDA
 TIR 489 LGTSNFKVSA SPLLTYLIEKTMQNVKHPV--TGQFLYQDSNWA SKV-EK
 PSMA 457 EGN YTLRVDCTPLMYSLVHNLTKELKSPDEGFEGKSLYESWTKKSPSPEF

TIR2-α 560 EVIRPLPMDSSAYSFTA FV--GVP--AVEFSFMEDDQAYPELHTKEDT
 TIR 535 LTLDNAAFPFLAYS-----GIP--AVSFCFCEDTD-YPYLGTTMDT
 PSMA 507 SGMPRISKLGSGNDFE VFFQRLGIASGRA RYTKNWE TNKFSGYPLYHSVY

TIR2-α 604 YENLHKVLQGR LPAVAQA--VAQLAGQLLIRLSHDLRLPLDFGRYGDVVL
 TIR 573 YKEL-IERIPELNKVARA--AAEVAGQFVIKLTHDVELNLDYERYNSQLL
 PSMA 557 ETYE-LVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFD CRDYAVVLR

TIR2-α 652 RHIGNLNEFSGLDK-ARGLTLQWVYSARGDYIRAAEKL RQEYSS EERDE
 TIR 620 SFVRDLNQYRADIK-EMGLSLQWLYSARGDFFRATSLT TDFGN-AEKTD
 PSMA 606 KYADKIYSISMKHPQEMKTSVSFDSLFS AVKNFT EIASKFSERLQDFDK

TIR2-α 701 RLTRMY--NVRIMRVEFYFLSQYVSPADSPF-RHIFMGRGDHTLGALLD
 TIR 668 RFV-MKKL-NDRVMRVEYHFLSPYVSPKESPF-RHVFWGSGSHTLPALLE
 PSMA 656 SNPIVLRMMNDQLMFLERA FIDPLGLPDR-PFYRHVITYAPSSH NKYAGES

TIR2-α 747 HLRLLRSNSSGTPGATSSTGFQESRFRRLQALALTWT LQGAANALSGDVWN
 TIR 715 NLKLRKQNN-----GAFNETLFRNLQALALTWT LQGAANALSGDVWD
 PSMA 705 FPGIYDALFDIESKVDPSKAWGEVK-R-QIYVA AFTVQAAAETLS-EVAD

TIR2-α 797 IDNNF
 TIR 756 IDNEF
 PSMA 752 I

FIG. 4A

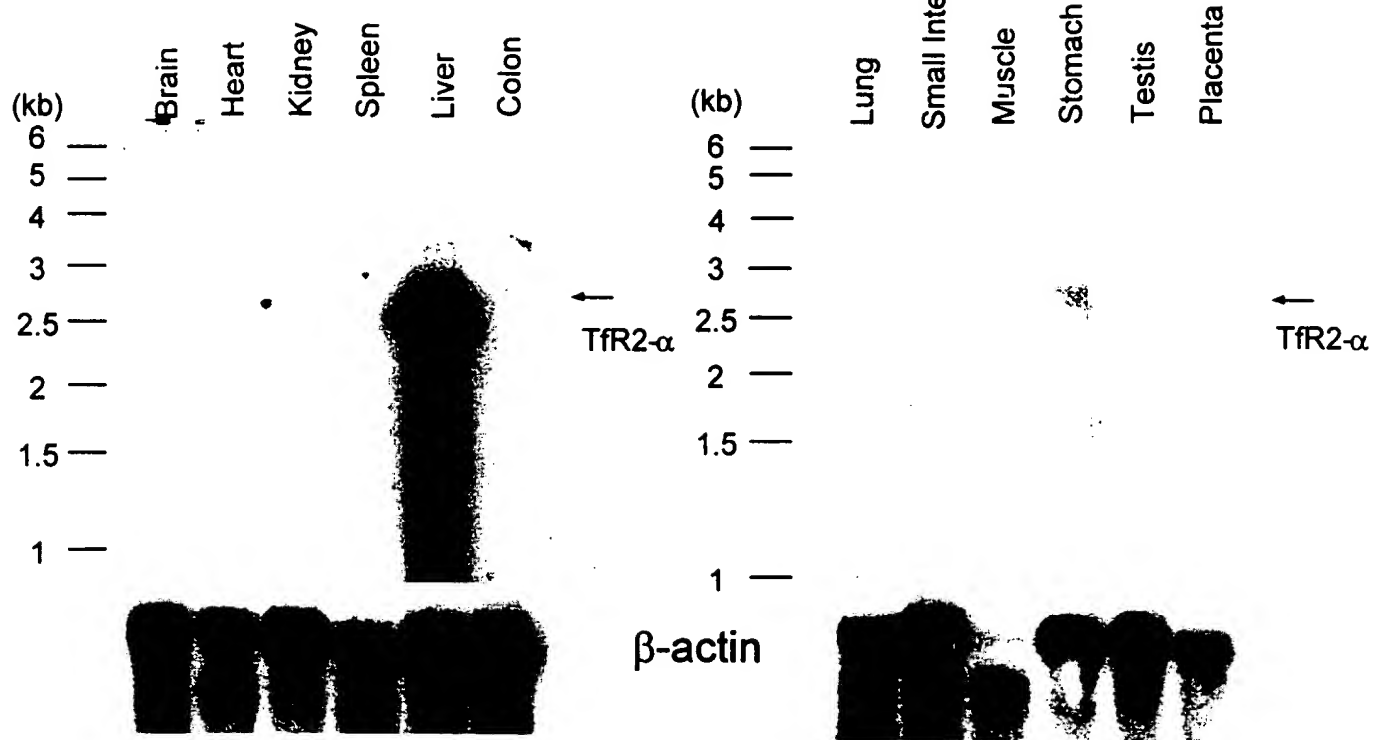


FIG. 4B

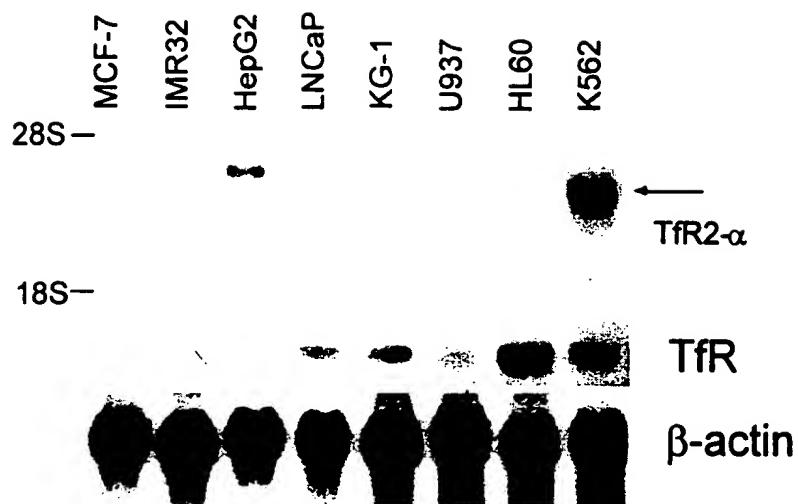


FIG. 5A

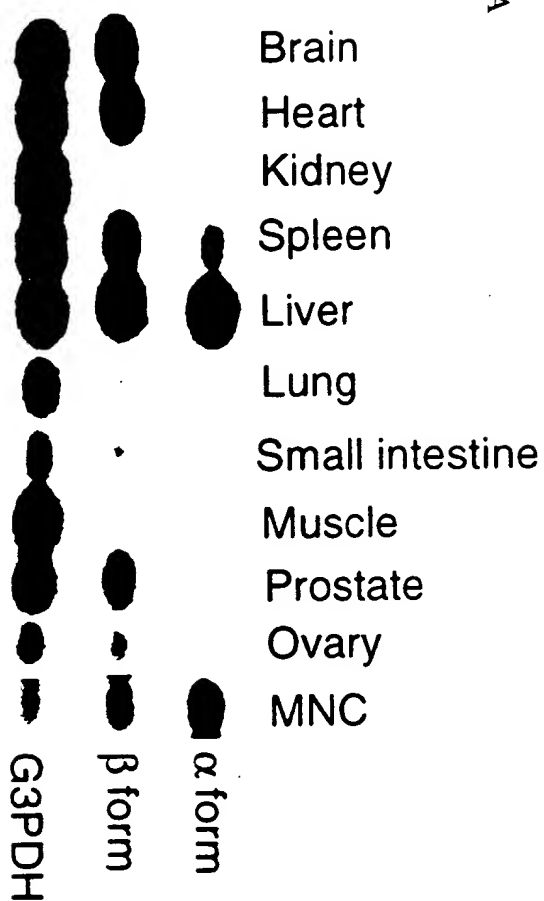


FIG. 5B

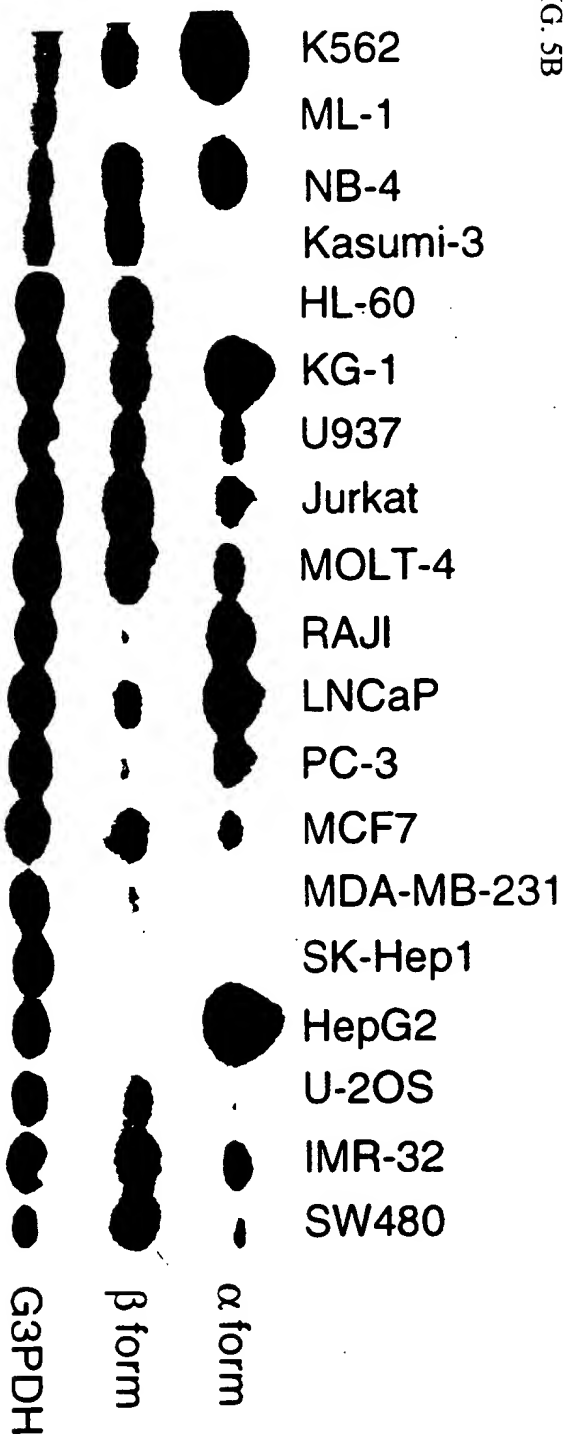


FIG. 6A

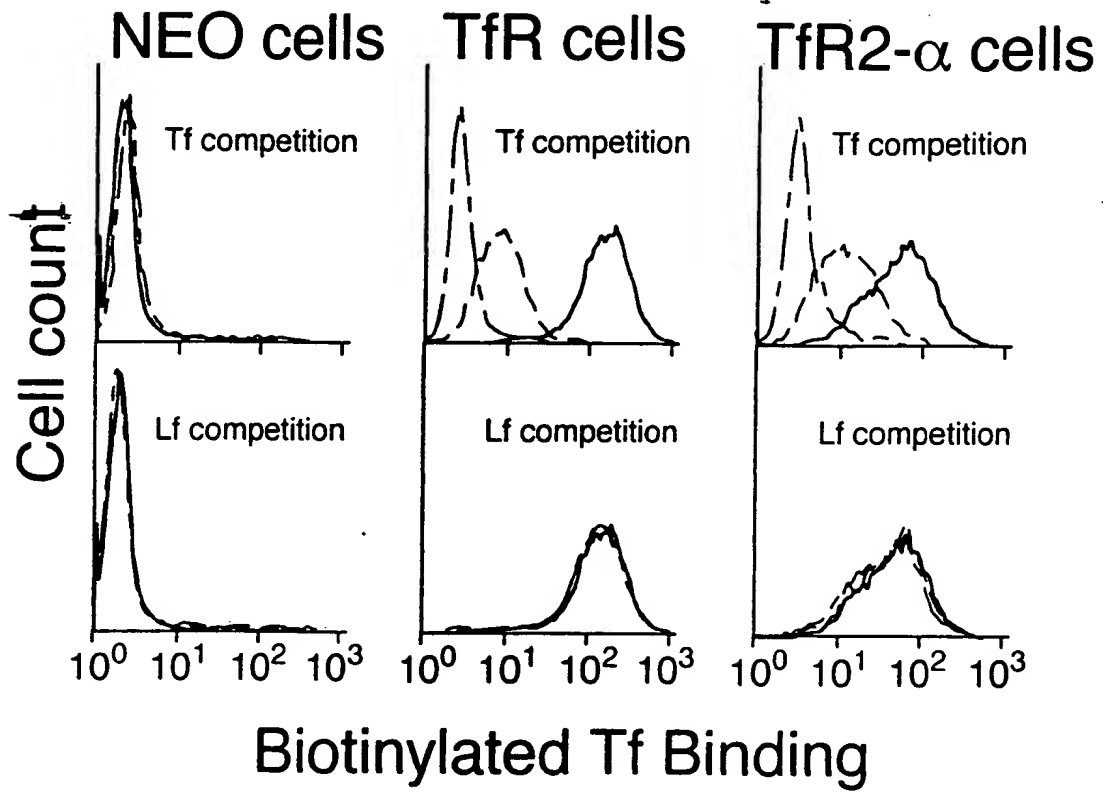


FIG. 6B

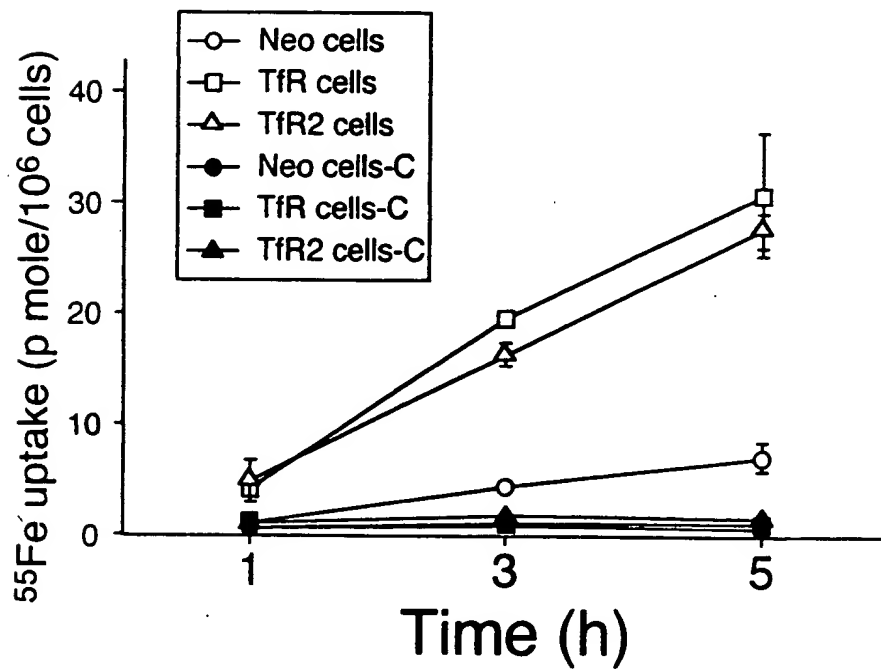


FIG. 6C

C

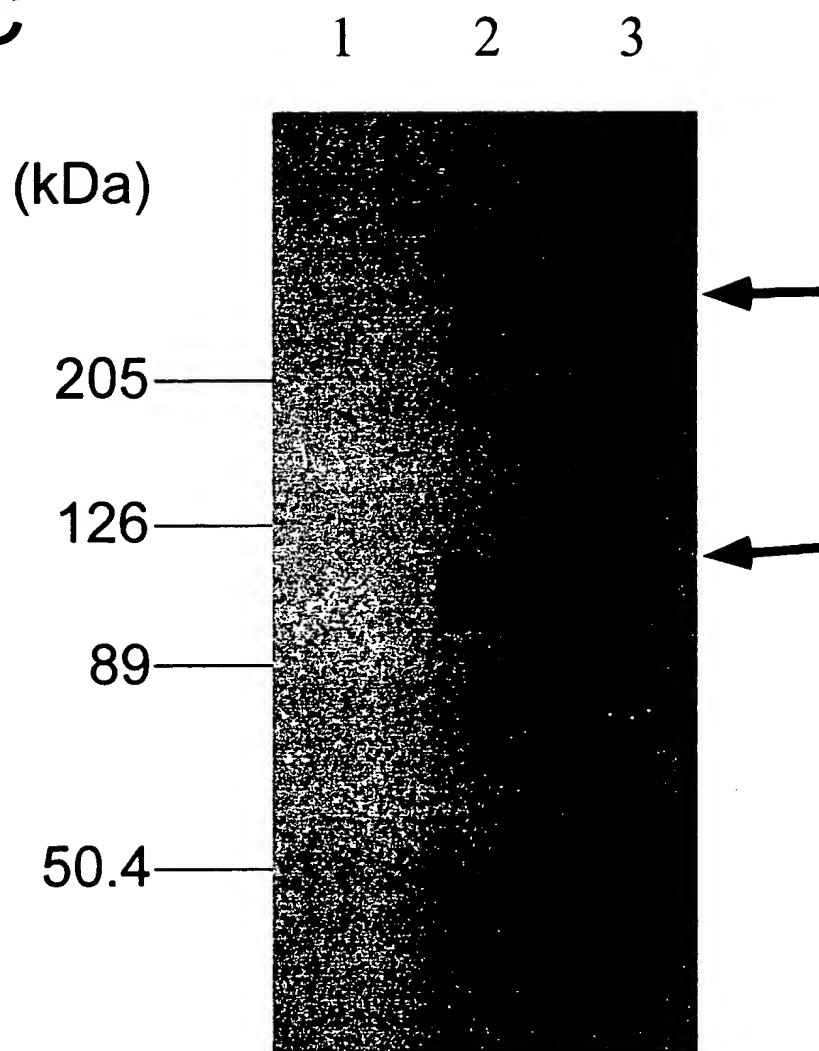


Fig. 7 alpha amino acid sequence

MERLWGLFQRAQQLSRSSQTVYQRVGPRKGHLEEEEDGEEGAETLAHFCPMELRGPEPLGSRPRQPNLI PWAAAGRR
AAPYLVL TALLIFTGAFLLGYVAFRGSCQACGDSVLVVS EDVNYEPDLDFHQGRLYWSDLQAMFLQFLGEGRLED TIRQT
SLRERVAGSAGMAALTQDIRAALS RQKLDHVWTDTHYVGLQFPDPAHPNTLHWVDEAGKVGEQLPLEDPDVYCPYSAIGN
VTGELVYAHYGRPEDLQDLRARGVDPVGRLLLV RVGVISFAQKVTNAQDFGAQGVLIYPEPADFSQDPPKPSLSSQQAVY
GHVHLGTGDPYTPGFPSFNQTQFPVASSGLPSIPAQPI SADIASRLRLKLGKGPVAPQEWQGSLLGSPYHLGPGPRLRLV
VNNHRTSTFINNIFGCI EGRSEPDHYVVIGAQRDAWGPGA AKSAVGTAI LLELVRTFSSMVSNGFRPRRSLLFISWDGGD
FGSVGSTEWLEGYLSVLHLKAVVYVSLDNAVLGDDKFHAKTSPLLTSLIESVLKQVDSPNHSGQTLYEQVVFTNPSWDAE
VIRPLPMDSSAYSFTA FVGVPAVEFSFMEDDQAYPFLHTKEDTYENLHKVLQGRLP AVAQAVAQLAGQLLIRLSHDRLLP
LDFGRYGDVVL RHIGNLNEFSGDLKARGLTLQWVYSARGDYIRAAEKLQEIYSSEERDERLTRMYNVRIMRVEFYFLSQ
YVSPADSPFRHIFMGRGDHTLGALLDHLRL LRSNSSGTPGATSSTGFQESRFRRLALLTWTLQGAANALSGDVWNIDNN
F

Fig. 3 alpha DNA sequence

CTGCAGGCTTCAGGAGGGGACACAAGCATGGAGCGGCTTTGGGGTCTATTCCAGAGAGcGCAACAACCTGTCCCCAAGATC
CTCTCAGACCGTCTACCAGCGTGTGGAAGGCCCCCGGAAAGGGCACCTGGAGGAGGAAGAGGAAGACGGGGAGGAGGGG
CGGAGACATTGGCCCCACTTCTGCCCCATGGAGCTGAGGGGGCCCTGAGCCCCCTGGGCTCTAGACCCAGGCAGCCAAACCTC
ATTCCCTGGCGCGCAGCAGGACGGAGGGCTGCCCCCTACCTGGTCTTGACGGCCCTGCTGATCTTCACTGGGGCCTTCCT
ACTGGGCTACGTGCGCTTCCGAGGGTCTGCCAGGCGTGCGGAGACTCTGTGTTGGTGGTCACTGAGGATGTCAACTATG
AGCCTGACCTGGATTTCCACCAGGGGcagactctactggaGcgacCtccaGgccaatgttctctgcagttccttgggggaGggg
cgccctggaGgaCaccaTCAGGCAAACCAGCCTTCGGGAACGGGTGGCAGGCTCGGCCGGGATGGCCGCTCTGACTCAGGA
CATTCGCGCGGGCGCTCTCCCGCCAGAAGCTGGACCACGTGTGGACCGACACGCACTACGTGGGGCTGCAATTCCCGGATC
CGGCTCACCCCCAACACCCTGCACTGGGTGATGAGGCCGGGAAGGTGCGAGAGCAGTGGCCGTGGAGGACCCTGACGTC
TACTGCCCTACAGcGCCATCGGCAACGTACGGGAGAGCTGGTGTAcGCCCACTACGGGCGGGCCGAAGACCTGCAGGA
CcTGCGGGCCAGGGGCGTGGATCCAGTGGGCCGCTGCTGCTGGTGGCGTGGGGGTGATCagcTTCCGCCAGAAGGTGA
CCAATGCTCAGGACTTCGGGGCTCAAGGAGTGTCTATATACCCAGAGCCAGCGGACTTCTCCAGGACCCACCCAAGCCA
AGCCTGTCCAGCCAGCAGGCAGTGTATGGACATGTGCACCTGGGAACCTGGAAGACCCcTACACACCTGGCTTCCTTTCCTT
CAATCAAACCCAGTTCCCTCCAGTTGCATCATCAGGCCCTTCCAGCATCCcAGCCCAGCCCATCAGTGCAGACATTGCCT
CCCGCTGCTGAGGAAGCTCAAAGGCCCTGTGGCCCCCAAGAATGGCAGGGGAGCCTCCTAGGCTCCCCCTTATCACCTG
GGCCCCGGGCCACGACTGCGGCTAGTGGTCAACAATCACAGGACCTCCACCCCATCAACAACATCTTCGGCTGCATCGA
AGGCGCTCAGAGCCAGATCACTACGTTGTCTCGGGGCCAGAGGGATGCATGGGGCCAGGAGCAGCTAAATCCGCTG
TGGGCGCTGCTATACTCCTGGAGCTGGTGGGACCTTTTCCCTCCATGGTGAGCAACGGCTTCCGGCCCCGAGAAGTCTC
CTCTTCATCAGCTGGGACGGTGGTGACTTTGGAAGCGTGGGCTCCACGGAGTGGCTAGAAGGTACCTCAGCGTGTGCA
CCTCAAAGCCGTAGTGTACGTGAGCCTGGACAACGCAGTGTGGGGATGACAAGTTTCATGCCAAGACCAGCCCCCTTC
TGACAAGTCTCATTGAGAGTGTCTGAAGCAGGTGGATTCTCCCAACCACAGTGGGCAGACTCTCTATGAACAGGTGGTG
TTCACCAATCCCAGCTGGGATGCTGAGGTGATCCGGCCCCTACCCATGGACAGCAGTGCCTATTCCTTCACGGCCTTTGT
GGGAGTCCCTGCCGTGAGTTCTCCTTTATGGAGGACGACCAGGCCCTACCCATTCTCTGCACACAAAGGAGGACACTTATG
AGAACCTGCATAAGGTGCTGCAAGGCCGCCTGCCGCCGTGGCCAGGCCGTGGCCAGCTCGCAGGGCAGCTCCTCATC
CGGCTCAGCCACGATCGCCTGCTGCCCCCTCGACTTCGGCCGCTACGGGGACGTCTCTCAGGCACATCGGGAACCTCAA
CGAGTTCTCTGGGGACCTCAAGGCCCCGCGGCTGACCTGCACTGGGTGTACTCGGCGCGGGGGACTACATCCGGGCGG
CGGAAAAGCTGCGGCAGGAGATCTACAGCTCGGAGGAGAGAGACGAGCGACTGACACGCATGTACAACGTGCGCATAATG
CGGGTGGAGTTCTACTTCCTTTCCAGTACGTGTGCGCAGCCGACTCCCCGTTCGCCACATCTTCATGGGCGGTGGAGA
CCACACGCTGGGCGCCCTGCTGGACCACCTGCGGCTGCTGCGCTCCAACAGCTCCGGGACCCCCGGGGCCACCTCCTCCA
CTGGCTTCAGGAGAGCCGTTTCCGGCGTCAGCTAGCCCTGCTCACCTGGACGCTGCAAGGGGCAGCCAATGCGCTTAGC
GGGGATGTCTGGAACATTGATAACAACCTTCTGAGGCCCTGGGGATCCTCACATCCCCGTCCCCAGTCAAGAGCTCCTCT
GCTCCTCGCTTGAATGATTCAAGGTGAGGGAGGTGGCTCAGAGTCCACCTCTCATTTGCTGATCAATTTCTCATTACCCCT
ACACATCTCTCCAGGAGCCCAGACCCAGCACAGATATCCACACACCCAGCCCTGCAGTGTAGCTGACCCTAATGTGA
CGGTCTACTGTGCGTTAATCAGAGAGTAGCATCCCTTCAATCACAGCCCCCTTCCCCTTTCTGGGGTCTCCATACCTAG
AGACCACTcTGGGAGGTTTGTAGGCCCTGGGACCTGGCCAGCTCTGTTAGTGGGAGAGATCGCTGGCACCATAGCCTTA
TGGCCAACAGGTGGTcTGTGGTGAAAGGGGCGTGGAGTTTCAATATCAATAAACACCTGATATCAATAAGCCAAAA

Fig. 9 beta DNA sequence

GCGTCCGCGGGGAGCGCTCTTTTCTAAACTCAGGAACCCCTCGCGCGCCCTGCCCTGGCGACCCACGTCTCTGGCAT
CCTTCCCTCTTCCCTCCCTCTCTCCGGGCGCCCAAAAAGTCCCCACCTCTCCCGCTTAGGCAAACCAGCCTTCGGGA
ACGGGTGGCAGGCTCGGCGGGGATGGCGCTCTGACTCAGGACATTTCGCGCGCGCTCTCCCGCCAGAAGCTGGACCACG
TGTGSACCSACAGCACTACGTGGGGCTGCAATTCCCGGATCCGGCTCACCCCAACACCCTGCACTGGGTGATGAGGCC
GGSAAGGTTCGGAGAGCAGCTGCGCTGGAGGACCCTGACGTCTACTGCCCCACAGCGCCATCGGCAACGTACGCGGAGA
GCTGGTGTAGCCCCACTACGGGCGGCCGAAGACCTGCAGGACCTGCGGGCCAGGGGCGTGGATCCAGTGGGCGCGCTGC
TGCTGGTGCCTGGGGGTGATCagcTTCGCCCAGAAGGTGACCAATGCTCAGGACTTCGGGGCTCAAGGAGTGCTCATA
TACCCAGAGCCAGCGACTTCTCCAGGACCCACCCAAGCCAAGCCTGTCCAGCCAGCAGGCAGTGATGGACATGTGCA
CCTGGGAACCTGGAGACCCcTACACACCTGGCTTCCCTTCTTCAATCAAACCCAGTTCCCTCCAGTTGCATCATCAGGCC
TTCCAGCATCCcAGCCAGCCCATCAGTGCAGACATTGCCTCCCGCTGCTGAGGAAGCTCAAAGGCCCTGTGGCCCCC
CAAGAATGGCAGGGGAGCCTCCTAGGCTCCCTTATACCTGGGCCCCGGGCCACGACTGCGGCTAGTGGTCAACAATCA
CAGGACCTCCACCCCCATCAACAACATCTTCGGCTGCATCGAAGGCCGCTCAGAGCCAGATCACTACGTTGTTCATCGGGG
CCCAGAGGGATGCATGGGGCCAGGAGCAGCTAAATCCGCTGTGGGGACGGCTATACTCCTGGAGCTGGTGCAGACCTTT
TCCTCCATGGTGAGCAACGGCTTCCGGCCCCGAGAAGTCTCCTCTTCATCAGCTGGGACGGTGGTGACTTTGGAAGCGT
GGGCTCCACGGAGTGGCTAGAAGGCTACCTCAGCGTGCTGCACCTCAAAGCCGTAGTGTACGTGAGCCTGGACAACGCAG
TGCTGGGGGATGACAAGTTTCATGCCAAGACCAGCCCCCTCTGACAAGTCTCATTGAGAGTGTCTGAAGCAGGTGGAT
TCTCCCAACCACAGTGGGCAGACTCTCTATGAACAGGTGGTGTTCACCAATCCCAGCTGGGATGCTGAGGTGATCCGGCC
CCTACCCATGGACAGCAGTGCCTATTCTTCACGGCCTTTGTGGGAGTCCCTGCCGTGAGTTCTCTTTATGGAGGACG
ACCAGGCCTACCCATTCTGCACACAAAGGAGGACACTTATGAGAACCTGCATAAGGTGCTGCAAGGCCGCTGCCGCC
GTGGCCAGGCCGTGGCCAGCTCGCAGGGCAGCTCCTCATCCGGCTCAGCCACGATCGCTGCTGCCCTCGACTTCGG
CCGCTACGGGGACGTCTCTCAGGCACATCGGGAACCTCAACGAGTTCTCTGGGGACCTCAAGCCCCGCGGGCTGACCC
TGCACTGGGTGTACTCGGCGCGGGGGGACTACATCCGGGCGGGCGGAAAAGCTGCGGCAGGAGATCTACAGCTCGGAGGAG
AGAGACGAGCGACTGACACGCATGTACAACGTGCGCATAATGCGGGTGGAGTTCTACTTCTTTCCAGTACGTGTGCC
AGCCGACTCCCCJTTCGGCCACATCTTCATGGGCGTGGAGACCACACGCTGGGCGCCCTGCTGGACCACCTGCGGCTGC
TGCGCTCCAACAGCTCCGGGACCCCCGGGGCCACCTCCTCCACTGGCTTCCAGGAGAGCCGTTTCCGGCGTCAGCTAGCC
CTGCTCACCTGGACGCTGCAAGGGGACGCCAATGCGCTTAGCGGGGATGTCTGGAACATTGATAACAACCTTCTGAGGCC
TGGGGATCCTCACATCCCCGTCCCCAGTCAAGAGCTCCTCTGCTCCTCGCTTGAATGATTCAGGGTCAGGGAGGTGGCT
CAGAGTCCACCTCTCATTGCTGATCAATTTCTCATTACCCCTACACATCTCTCCACGGAGCCCAGACCCAGCACAGATA
TCCACACACCCAGCCCTGCAGTGTAGCTGACCTAATGTGACGGTCATACTGTGCGTTAATCAGAGAGTAGCATCCCTT
CAATCACAGCCCCCTTCCCTTTCTGGGGTCTCCATACCTAGAGACCACTcTGGGAGGTTTGTAGGCCCTGGGACCTGG
CCAGCTCTGTAGTGGGAGAGATCGCTGGCACCATAGCCTTATGGCCAACAGGTGGTcTGTGGTGAAAGGGGCGTGGAGT
TTCAATATCAATAAACCACCTGATATCAATAAGCCAAAA